

SEQUENCE LISTING



APR 11 2000

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Rotkreuzstiftung Zentrallaboratorium  
Blutspendedienst
- (B) STREET: Wankdorfstrasse 10
- (C) CITY: Bern 22
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE (ZIP): CH-3000

(ii) TITLE OF INVENTION: Recombinant Fab-fragment with reactivity  
against Rhesus D antigens, DNA encoding them, complete  
antibodies comprising the Fab fragments and process for  
their preparation

(iii) NUMBER OF SEQUENCES: 64

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/EP97/03253

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: EP 96810421.6
- (B) FILING DATE: 24-JUN-1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: Adult
- (E) HAPLOTYPE: Diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA Library, LD1
- (B) CLONE: LD1-40

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: Chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..342)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG

48

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

TCC CTG AGA CTC TCC TGT ATA GCG TCT GGA TTC ACC CTC AGG AAT TAT

96

Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr

20 25 30

GCC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG

144 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

GCA GGT ATA TGG TTT GAT GGA AGT AAC AAA AAC TAT GCA GAC TCC GTG  
192

Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val  
50 55 60

AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT  
240

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

CTG CAA CTG AAC AGC CTG AGA GAC GAG GAC ACG GCT GTG TAT TAT TGT  
288

Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

GCG AGA GAG CGA GCA GCA CGT GGT ATT TCT AGG TTC TAT TAC TAC ATG  
336

Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met  
100 105 110

GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC CCA 375  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Pro  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Pro  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: Adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1
- (B) CLONE: LD1-40

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: Chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..318
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION:join(64..96, 142..162, 259..288)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGC GAC AGA  
48

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGG AGC CAT TTG AAT  
96

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn  
20 25 30

TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG TTG CTG ATC TAT GGT  
144

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly  
35 40 45

GCG TCC ACT TTG CAA AGT GGC GTC CCA TCA AGG TTC AGT GGC AGT GGC  
192

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

TCT GGG GCA GTT TTC ACT CTC ACC ATC GCC AGT CTA CAA CCT GAA GAT  
240

Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp  
65 70 75 80

TTT GCA ACT TAC TAC TGT CAA GAG AGT TAC AGT AAT CCT CTA ATC ACC  
288

Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr  
85 90 95

TTC GGC CAA GGG ACA CGA CTG GAG ACT AAA 318  
Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn  
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly  
35 40 45

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr  
85 90 95

Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: Adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1
- (B) CLONE: LD1-52

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: Chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..375
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION:join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG  
48

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly

1 5 10 15

TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC GCC CTC AGA AGT TCT  
96

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser

20 25 30

GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG  
144

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG  
192

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val  
50 55 60

AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT  
240

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr  
65 70 75 80

CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT  
288

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG  
336

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 375  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 318 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  - (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
  - (D) DEVELOPMENTAL STAGE: Adult
  - (E) HAPLOTYPE: Diploid
  - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA Library, LD1
  - (B) CLONE: LD1-52
- (viii) POSITION IN GENOME:
  - (A) CHROMOSOME/SEGMENT: Chromosome 2
  - (B) MAP POSITION: P 11

(C) UNITS: chromosome b.No

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..318
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION:join(64..96, 142..162, 259..288)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA  
48

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT ATC CGC TAT TTA AAT  
96

Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn  
20 25 30

TGG TAT CAG CAG AAG CCA GGG AAA GCC CCT AGG CTC CTG ATC TAT GGT  
144

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly  
35 40 45

GCG TCC ACT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA  
192

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

TCT GGG ACA GAT TTC ACT CTC ACC ATC AGT AGT CTG CAA CCT GAA GAT  
240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC CGT ACC CCT CCA TTC ACT  
288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr  
85 90 95

Phe Gly Pro Gly Thr Lys Val Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn  
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly  
35 40 45

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr  
85 90 95

Phe Gly Pro Gly Thr Lys Val Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: Adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA LIBRARY, LD1
- (B) CLONE: LD1-84

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: Chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION:join(91..105, 148..198, 295..342)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..375
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG  
48

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT  
96

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser  
20 25 30

GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG

144

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG  
192

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val  
50 55 60

AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT  
240

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr  
65 70 75 80

CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT  
288

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG  
336

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 375  
Asp Val Trp Gly Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser  
20 25 30

APR 11 2000

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune rhesus D donor
- (D) DEVELOPMENTAL STAGE: Adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA LIBRARY, LD1
- (B) CLONE: LD1-84

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: Chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA GGA GAC AGA

48

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg

1 5 10 15

GTC ACC ATC ACC TGC CGG GCA AGT CAG AGT ATC ATC AGG TAT TTG AAT

96

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn

20 25 30

TGG TAT CAG CAC AAA CCA GGA AAA GCC CCT AAA CTC CTC ATC TTT GCT

144

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala

35 40 45

GCA TCG AAT TTG CAA ACT GGG GTC CCA TCC AGG TTC AGT GGC AGT GGA

192

Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly

50 55 60

TCT GGG ACA GAT TTC ACT CTC ACC ATC AGT GAC CTG CAG CCT GAG GAT

240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp

65 70 75 80

TTC GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT AGG CCG TTC ACT TTT

288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe

85

90

95

GGC CGG GGG ACC AGC CTG GAC ATC AAA  
Gly Arg Gly Thr Ser Leu Asp Ile Lys  
100 105

315

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg  
1 . 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn  
20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala  
35 40 45

Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe  
85 90 95

Gly Arg Gly Thr Ser Leu Asp Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA LIBRARY, LD1
- (B) CLONE: LD1-110

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: Chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..348)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG

48

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

TCC CTG AGA CTC TCC TGT ATA GCG TCT GGA TTC ACC CTC AGG AAT TAT 96

Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr

20 25 30

GCC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG

144

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35            40            45

GCA GGT ATA TGG TTT GAT GGA AGC AAC AAA AAC TAT GCA GAC TCC GTG

192

Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val  
50            55            60

AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC TCC AAG AAC ACT CTG TTT

240

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe  
65            70            75            80

CTG CAC ATG AAC AGC CTG AGA GCC GAG GAC ACG GCT ACA TAT TAC TGT

288

Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys  
85            90            95

GCG AGA GAG AGG GCG ATT CGG GGA ATC AGT AGA TAC AAT TAC TAC ATG

336

Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100            105            110

GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA            375

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser

115            120            125

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1            5            10            15

Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr

20            25            30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe  
65 70 75 80

Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys  
85 90 95

Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: Adult
- (E) HAPLOTYPE: Diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA Library, LD1
- (B) CLONE: LD1-110

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: Chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: chromosome b.No

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA

48

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

1 5 10 15

GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT CGA AGC TCT TTA AAT

96

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn

20 25 30

TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAA GTC CTG ATC TAT GCT

144

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala

35 40 45

GCA TCC AGT TTG CAA AGT GGG GTC CCA TCC AGG TTC AGT GGC AGA GGA

192

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly

50 55 60

TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAG CCT GAA GAT

240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp

65 70 75 80

TTT GCG ACT TAT TAT TGT CAA CAG AGT TCC AGT TCC TCG TGG ACG TTC

288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Trp Thr Phe

85

90

95

GGC CAA GGG ACC AAG GTG GAA ATC AAA  
Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

315

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn  
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala  
35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Trp Thr Phe  
85 90 95

Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA LIBRARY, LD1
- (B) CLONE: LD1-117

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: Chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..345)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CAG GTG AAA CTG CTC GAG TCA GGA GGA GGC GTG GTC CAG CCT GGG AAG

48

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Lys

1 5 10 15

TCC CTG AGA CTT TCC TGT GCA GCG TCT GGA TTC AGT TTC AAT AGC CAT 96

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ser His

20 25 30

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG

144

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

GCA TTT ATA TGG TTT GAT GGC AGT AAT AAA TAC TAT GCA GAC TCC GTG

192

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

AAG GGC CGA TTC ACC ATC ACC AGA GAC AAC TCC AAG AAC ACG CTG TAT

240

Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC ACG GCT GTC TAT TAC TGT

288

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

GCG AGA GAG ACC TCA GTA AGG CTA GGG TAT AGC CGC TAC AAT TAC TAC

336

Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr  
100 105 110

ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC ATC TCG TCA

378

Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Ile Ser Ser

115 120 125

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Lys  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ser His  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr  
100 105 110

Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Ile Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 318 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  - (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
  - (D) DEVELOPMENTAL STAGE: adult
  - (E) HAPLOTYPE: diploid
  - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA LIBRARY, LD1
  - (B) CLONE: LD1-117

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: Chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..288)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA

48

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

1 5 10 15

GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGG AGC CAT TTG AAT

96

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn

20 25 30

TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT

144

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala

35 40 45

GCA TCC AGT TTG CAA GGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA

192

Ala Ser Ser Leu Gln Gly Val Pro Ser Arg Phe Ser Gly Ser Gly

50 55 60

TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT

240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp

65 70 75 80

TTT GCA ACT TAT TAC TGT CAA CAG AGT TAC AGG GCC CCT CAG TGG ACG

288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr

85

90

95

TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA  
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

318

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn  
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45

Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr  
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA LIBRARY, LD2
- (B) CLONE: LD2-1

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG

48

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly

1 5 10 15

TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC CTC AGG AGT TAT 96

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr

20 25 30

APR 11 2000

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG

144

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG

192

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val

50 55 60

AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG GTC TAT

240

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr

65 70 75 80

CTG CAA ATG AAC AGC CTG AGA GCC GAT GAC ACG GCT GTA TAT TAT TGT

288

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

GCG AGA GAG AAG GCG CTT CGG GGA ATC AGC AGA TAC AAC TAT TAC CTG

336

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu

100 105 110

GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA

375

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser

115 120 125

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmund Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA LIBRARY, LD2  
(B) CLONE: LD2-1

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: chromosome 22  
(B) MAP POSITION: q11  
(C) UNITS: Chromosome band number

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..333  
(D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3  
(B) LOCATION: join(61..99, 145..165, 262..294)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGA CAG AGG GTC  
48  
Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val  
1 5 10 15

ACC ATC TCT TGT TCT GGA AGC AAC TCC ATC CTT GGA AGT AAG TAT GTA  
96  
Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val  
20 25 30

TAC TGG TAC CAG AAA CTC CCA GGA ACG GCC CCC AAA CTC CTC ATC TAT  
144  
Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Ile Tyr  
35 40 45

AAG AAT GAT CAG CGG CCC TCA GGG GTC TCT GAC CGA TTC TCT GGC TCC  
192  
Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser  
50 55 60

AAG TCT GGC ACC TCG GCC TCC CTG GCC ATC AGT GGG CTC CGG TCC GAG  
240  
Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu  
65 70 75 80

GAT GAG GCT GAC TAT TAC TGT GCA CCA TGG GAT GCC AAC CTG GGT GGC  
288

Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly  
85 90 95

CCG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA AGT CAG CCC 333  
Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro  
100 105 110

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val  
1 5 10 15

Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val  
20 25 30

Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Ile Tyr  
35 40 45

Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser  
50 55 60

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu  
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly  
85 90 95

Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro  
100 105 110

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA Library, LD2
- (B) CLONE: LD2-4

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..375
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION:join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG GGG

48

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly

1 5 10 15

TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT

96

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser  
20 25 30

GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG

144

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG

192

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val  
50 55 60

AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT

240

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr  
65 70 75 80

CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT

288

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG

336

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 375

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser

115 120 125

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid

(G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-4

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..282)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA

48

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

1 5 10 15

GTC ACC ATC ACT TGC CGG ACA AGT CAG ACC ATT AGC AGA AAT TTA AAT

96

Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn

20 25 30

TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT

144

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala

35 40 45

ACA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA

192

Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly

50 55 60

TCT GGG ACA GAT TTC ACT CTC ACC ATC AAT AGT CTA CAA CCT GAA GAT

240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp  
65 70 75 80

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC ACT ACC CCT TCG TTC GGC  
288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly  
85 90 95

CAA GGG ACC AAG GTG GAA ATC AAA 312  
Gln Gly Thr Lys Val Glu Ile Lys  
100

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn  
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45

Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly  
85 90 95

Gln Gly Thr Lys Val Glu Ile Lys  
100

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-4

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTC CAG CCG GGG GGG

48

Gln Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AGT TAT 96  
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr  
20 25 30

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG  
144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG  
192  
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
50 55 60

AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG CTC TAT  
240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr  
65 70 75 80

CTG CAA ATG AAT AGC CTG AGA GCC GAG GAC ACG GCT GTA TAT TAT TGT  
288  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

GCG AGA GAG AAG GCG CTT CGG GGA ATC AGT AGA TAC AAC TAT TAC CTG  
336  
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
100 105 110

GAC GTC TGG GGC AAG GGG GCC ACG GTC ACC GTC TCC TCA 375  
Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Gln Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
100 105 110

Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDND library. LD2
- (B) CLONE: LD2-5

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..288)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA GGC GAC AGA  
48  
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg  
1 5 10 15

GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC GTT ACC AGG TCT TTA AAT  
96  
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn  
20 25 30

TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AGG CTC CTA ATC TTT GCT  
144  
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala  
35 40 45

GCG TCC ACT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA  
192  
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

TCT GGG ACA GAT TTC ACC CTC ACC ATC AGC AGT CTG CAA CCT GAG GAT  
240  
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

TTT GGA ACT TAC TAC TGT CAA CAG AAT TAC AGG ACC CCT CAG TGG ACG  
288

Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr  
85 90 95

TTC GGC CAA GGG ACC AAG GTA GAA ATC AAA 318  
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn  
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala  
35 40 45

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr  
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-10

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..378
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION:join(91..105, 148..198, 298..345)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG

48

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly

1

5

10

15

TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC CTC AGG AGT TAT 96  
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr  
20 25 30

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG  
144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG  
192  
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
50 55 60

AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG GTC TAT  
240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr  
175 180 185

CTG CAA ATG AAC AGC CTG AGA GCC GAT GAC ACG GCT GTA TAT TAT TAT  
288  
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr  
85 90 95

TGT GCG AGA GAG AAG GCG CTT CGG GGA ATC AGC AGA TAC AAC TAT TAC  
336  
Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr  
100 105 110

CTG GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 378  
Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr  
85 90 95

Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr  
100 105 110

Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-10

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 22
- (B) MAP POSITION: q11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..333
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(61..102, 148..168, 265..294)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GTG GTG ACT CAG GAG CCC TCA CTG ACT GTG TCC CCA GGA GGG ACA GTC  
48  
Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val  
1 5 10 15

ACT CTC ACC TGT GCT TCC AGC ACT GGG GCA GTC ACC AGG GGT TAC TAT  
96  
Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr  
20 25 30

CCA AAC TGG TTC CAG CAG AAG CCT GGA CAA GCA CCC AGG GCA CTG ATT  
144  
Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile  
35 40 45

TAT AGT ACA AAC AAA AAA CAC TCC TGG ACC CCT GCC CGG TTC TCA GGC  
192  
Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly  
50 55 60

TCC CTC CTT GGG GGC AAA GCT GCC CTG ACA CTG TCA GGT GTG CAG CCT  
240  
Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro  
65 70 75 80

GAA GAC GAG GCT GAA TAT TAC TGC CTG CTC TAC TAT GGT GGT GCT CAA

288

Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln  
85 90 95

CTC GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA CGT CAG CCC 333  
Leu Val Phe Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro  
100 105 110

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val  
1 5 10 15

Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr  
20 25 30

Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile  
35 40 45

Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly  
50 55 60

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro  
65 70 75 80

Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln  
85 90 95

Leu Val Phe Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro  
100 105 110

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-11

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..375
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION:join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG GGG

48

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly

1

5

10

15

TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT  
96

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser  
20 25 30

GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG  
144

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG  
192

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val  
50 55 60

AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT  
240

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr  
65 70 75 80

CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT  
288

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG  
336

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 375  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid

(G) CELL TYPE: lymphocyte

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-11

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GTG TTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA CGA GAC AGA

48

Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg

1 5 10 15

GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT GGC AGT TAT TTA AAT

96

Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn

20 25 30

TGG TAT CAG CAC AAA CCA GGG ACA GCC CCT AAA CTC CTG ATC TAT GCT

144

Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala

35 40 45

GTA TCC GCT TTG CAA AGT GGG GTC CCA TCG AGG TTC AGT GGC AGT AGA

192

Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg

50 55 60

TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT

240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT CCC CCG TAC ACT TTC  
288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe  
85 90 95

GGC CAG GGG ACC AAC CTG CAG ATC AAA 315  
Gly Gln Gly Thr Asn Leu Gln Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn  
20 25 30

Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45

Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe  
85 90 95

Gly Gln Gly Thr Asn Leu Gln Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-14

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..375
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION:join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG  
48

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly

1

5

10

15

TCC CTG AGA GTC GCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AAT TTT 96  
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe  
20 25 30

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG  
144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

GCT TTT ATT TGG TTT GAT GCA AGT AAT AAA GGA TAT GGA GAC TCC GTT  
192  
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val  
50 55 60

AAG GGC CGA TTC ACC GTC TCC AGA GAC AAT TCC AAG AAC ACG CTC TAT  
240  
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

CTG CAA ATG AAC GGC CTG AGA GCC GAA GAC ACG GCT GTA TAT TAT TGT  
288  
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

GCG AGA GAG AAG GCG GTT CGG GGA ATT AGT AGA TAC AAC TAC TAC ATG  
336  
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 375  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly

1 5 10 15  
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe  
20 25 30  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 315 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
  - (D) DEVELOPMENTAL STAGE: adult
  - (E) HAPLOTYPE: diploid
  - (G) CELL TYPE: lymphocyte

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-14

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA GAC AGA  
48  
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AAC AAT TTA AAT  
96  
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn  
20 25 30

TGG TAT CAG CAG AAA CCA GGC AAA GCC CCT GAA CTC CTG ATC TAT GCT  
144  
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala  
35 40 45

GCA TCC AGT TTG CAA AGT GGG GTC CCT TCA AGG TTC CGT GGC AGT GGA  
192  
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly  
50 55 60

TCT GGG AGA GAT TTC ACT CTC ACC GTC ACC AGT CTG CAA CCT GAA GAT  
240  
Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp  
65 70 75 80

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CTG TGG ACG TTC  
288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe  
85 90 95

GGC CAA GGG ACC AAG GTG GAA ATC AAA 315  
Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn  
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala  
35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly  
50 55 60

Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe  
85 90 95

Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library
- (B) CLONE: LD2-17

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 14
- (B) MAP POSITION: q32.43
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG

48

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly

1

5

10

15

TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AGT TAT 96  
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr  
20 25 30

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG  
144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG  
192  
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
50 55 60

AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ACG CTC TAT  
240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

CTG CAA ATG AAG AGC CTG AGA GCC GAG GAC ACG GCT GTA TAT TAT TGT  
288  
Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

GCG AGA GAG AAG GCG CTT CGG GGA ATC AGT AGA TAC AAC TAT TAC CTG  
336  
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
100 105 110

GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 375  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly

1 5 10 15

APR 11 2000

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-17

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTG ATG ACC CAG TCT CCA TTC TCC CTG TCT GCA TCT GTA GGA GAC AGA  
48  
Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT AGG AGT TTT TTA AGT  
96  
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser  
20 25 30

TGG TAT CAG CAG AAA CCA GGG ACA GCC CCT AAG CTC CTG ATC TAT GCT  
144  
Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45

GCA TCC AGG TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGG  
192  
Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC ACT CTG CAA CCT GAA GAT  
240  
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp  
65 70 75 80

TTT GCG ACT TAC TAC TGT CAA CAG AGT TAC GCC CCT TGG ACG TTC

288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe  
85 90 95

GGC CAA GGG ACC AAG CTG GAA ATC AAA

315

Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg

1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser

20 25 30

Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala

35 40 45

Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly

50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp

65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe

85 90 95

Gly Gln Gly Thr Lys Leu Glu Ile Lys

100 105

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library LD2
- (B) CLONE: LD2-20

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG

48

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly

1 5 10 15

TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC TCC AGG AGT TAT 96  
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr  
20 25 30

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG  
144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
50 55 60

GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG  
192  
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
65 70 75 80

AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ACG CTC TAT  
240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
85 90 95

CTG CAA ATG AAG AGC CTG AGA GCC GAG GAC ACG GCT GTA TAT TAT TGT  
288  
Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
100 105 110

GCG AGA GAG AAG GCG CTT CGG GGA ATC AGT AGA TAC AAC TAT TAC CTG  
336  
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
205 210 215

GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 375  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-20

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA  
48  
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AGC TAT TTA AAT  
96  
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn  
20 25 30

TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT  
144  
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45

GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA  
192  
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT  
240  
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CGA TTC ACT TTC

288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe  
85 90 95

GGC CCT GGG ACC AAA GTG GAT ATC AAA

315

Gly Pro Gly Thr Lys Val Asp Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn

20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala

35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly

50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp

65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe

85 90 95

Gly Pro Gly Thr Lys Val Asp Ile Lys

100 105

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1
- (B) CLONE: LD1-6-17

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..384
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..351)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG

48

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

TCC CTG AGA CTT TCC TGT GCA GCG TCT GGA TTT ACC TTC AGT AGC TAT 96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG  
144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

GCA GAT ATA TGG TTT GAT GGA GGT AAT AAA CAT TAT GCA GAC TTC GTG  
192  
Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val  
50 55 60

AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG GTG TAT  
240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr  
65 70 75 80

CTA CAA ATG AAC AGC CTG AGA GTC GAG GAC ACG GCT GTG TAT TAC TGT  
288  
Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

GCG AGG GAT TAC TAT AGC GTT ACT AAG AAA CTC AGA CTC CAC TAC TAC  
336  
Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr  
100 105 110

TAC TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA  
384  
Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
220 225 230

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr  
100 105 110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult

(E) HAPLOTYPE: diploid  
(G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: cDNA library, LD1  
(B) CLONE: LD1-6-17

(viii) POSITION IN GENOME:  
(A) CHROMOSOME SEGMENT: chromosome 2  
(B) MAP POSITION: p11  
(C) UNITS: Chromosome band number

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..315  
(D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:  
(A) NAME/KEY: CDR1, CDR2, CDR3  
(B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA  
48

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT AGA AAT GAT TTA ACC  
96

Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr  
20 25 30

TGG TAT CAG CAA AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT  
144

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45

GCA TCC AAT TTA CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA  
192

Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

TCT GGC ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT GAA GAT

240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

TTT GCA ACT TAT TAC TGT CTA CAA GAT AAC AAT TTC CCG TAC ACT TTT 288  
Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe  
85 90 95

GGC CAG GGG ACC AAG CTG GAG ATC AAA 315  
Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr  
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45

Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe  
85 90 95

Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1 and LD2
- (B) CLONE: LD1/2-6-3

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG

48

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly

APR 11 2000

1 5 10 15

TCC CTG AGA GTC GCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AAT TTT 96  
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe  
20 25 30

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG  
144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

GCT TTT ATT TGG TTT GAT GCA AGT AAT AAA GGA TAT GGA GAC TCC GTT  
192  
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val  
50 55 60

AAG GGC CGA TTC ACC GTC TCC AGA GAC AAT TCC AAG AAC ACG CTC TAT  
240  
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

CTG CAA ATG AAC GGC CTG AGA GCC GAA GAC ACG GCT GTA TAT TAT TGT  
288  
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

GCG AGA GAG AAG GCG GTT CGG GGA ATT AGT AGA TAC AAC TAC TAC ATG  
336  
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 375  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid

(G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1 and LD2
- (B) CLONE: LD1/2-6-3

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA  
48

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AGA TAT TTA AAT  
96

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn  
20 25 30

TGG TAT CAG CAC AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC CAT ACT  
144

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr  
35 40 45

GCA TCC AGT TTG CAA AGT GGG GTC CCG TCA AGG TTC AGT GGC AGT GTA  
192

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val  
50 55 60

TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT

240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC ACT ACC CCG TAC ACT TTT

288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe  
85 90 95

GGC CAG GGG ACC AAG CTG CAG ATC AAA

315

Gly Gln Gly Thr Lys Leu Gln Ile Lys

100 105

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn  
20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr  
35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe  
85 90 95

Gly Gln Gly Thr Lys Leu Gln Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1 and LD2
- (B) CLONE: LD1/2-2-33

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG

48

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

TCC CTG AGA GTC GCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AAT TTT 96  
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe  
20 25 30

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG  
144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

GCT TTT ATT TGG TTT GAT GCA AGT AAT AAA GGA TAT GGA GAC TCC GTT  
192  
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val  
50 55 60

AAG GGC CGA TTC ACC GTC TCC AGA GAC AAT TCC AAG AAC ACG CTC TAT  
240  
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

CTG CAA ATG AAC GGC CTG AGA GCC GAA GAC ACG GCT GTA TAT TAT TGT  
288  
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

GCG AGA GAG AAG GCG GTT CGG GGA ATT AGT AGA TAC AAC TAC TAC ATG  
336  
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 375  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (C) INDIVIDUAL ISOLATE: hyperimmune Resus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA library, LD1 and LD2
  - (B) CLONE: LD1/2-6-33

- (viii) POSITION IN GENOME:
  - (A) CHROMOSOME SEGMENT: chromosome 2
  - (B) MAP POSITION: p11
  - (C) UNITS: Chromosome band number

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..315
  - (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

- (ix) FEATURE:
  - (A) NAME/KEY: CDR1, CDR2, CDR3
  - (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GTG ATG ACC CAG TCT CCA TCC TTC CTG TCT GCA TCT GTA GGA GAC AGA  
48  
Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AGA TAT TTA AAT  
96  
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn  
20 25 30

TGG TAT CAG CAC AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC CAT GCT  
144  
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala  
35 40 45

GCA TCC AGT TTG CAA AGT GGG GTC CCG TCA AGG TTC AGT GGC AGT GTA  
192  
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val  
50 55 60

TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT  
240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC ACT ACC CCG TAC ACT TTT  
288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe  
85 90 95

GGC CAG GGG ACC AAG CTG CAG ATC AAA 315  
Gly Gln Gly Thr Lys Leu Gln Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn  
20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala  
35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe  
85 90 95

Gly Gln Gly Thr Lys Leu Gln Ile Lys  
100 105